

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant must provide:**

- ☒ An ~~initial or~~ substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123  
For CRF submission help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

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#8



1638

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/643,755B

DATE: 01/23/2002

FEB 06 2002

TIME: 17:11:35

TECH CENTER 1600/2900

Input Set : A:\Sequence

Output Set: N:\CRF3\01232002\I643755B.raw

ENTERED

4 <110> APPLICANT: van Rooijen, Gijs  
 5 Keon, Richard Glenn  
 6 Boothe, Joseph  
 7 Shen, Yin  
 9 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants  
 11 <130> FILE REFERENCE: 9369-153  
 13 <140> CURRENT APPLICATION NUMBER: 09/643,755B  
 14 <141> CURRENT FILING DATE: 2000-08-23  
 16 <160> NUMBER OF SEQ ID NOS: 4  
 18 <170> SOFTWARE: PatentIn Ver. 2.0  
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 34 caa tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct 96  
 35 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro  
 36 20 25 30  
 38 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt 144  
 39 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu  
 40 35 40 45  
 42 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac 192  
 43 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr  
 44 50 55 60  
 46 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat 240  
 47 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp  
 48 65 70 75 80  
 50 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc 288  
 51 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe  
 52 85 90 95  
 54 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc 336  
 55 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile  
 56 100 105 110  
 58 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga 384  
 59 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg  
 60 115 120 125  
 62 aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac 432

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66 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc 480
67 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
68 145      150      155      160
70 tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa 528
71 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
72      165      170      175
74 cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg 576
75 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
76      180      185      190
78 gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac 624
79 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
80      195      200      205
82 atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg 672
83 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
84      210      215      220
86 gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca 720
87 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
88 225      230      235      240
90 tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag 768
91 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
92      245      250      255
94 tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt 816
95 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
96      260      265      270
98 gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag 864
99 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
100      275      280      285
102 ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga 912
103 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
104      290      295      300
106 gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt 960
107 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
108 305      310      315      320
110 agc tac atg oct aca gtt gtc ttt gag atc aac ggc aag atg tac cca 1008
111 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
112      325      330      335
114 ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt 1056
115 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
116      340      345      350
118 gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg 1104
119 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
120      355      360      365
122 ttc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt 1152
123 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
124      370      375      380
126 ggg cta gct aaa gca atc tga 1173
127 Gly Leu Ala Lys Ala Ile

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133 <212> TYPE: PRT
134 <213> ORGANISM: Bovine
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138 1 5 10 15
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141 20 25 30
143 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
144 35 40 45
146 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
147 50 55 60
149 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
150 65 70 75 80
152 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
153 85 90 95
155 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
156 100 105 110
158 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
159 115 120 125
161 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
162 130 135 140
164 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
165 145 150 155 160
167 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
168 165 170 175
170 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
171 180 185 190
173 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
174 195 200 205
176 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
177 210 215 220
179 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
180 225 230 235 240
182 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
183 245 250 255
185 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
186 260 265 270
188 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
189 275 280 285
191 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
192 290 295 300
194 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
195 305 310 315 320
197 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
198 325 330 335
200 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser

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203 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
204          355          360          365
206 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
207          370          375          380
209 Gly Leu Ala Lys Ala Ile
210 385          390
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 3957
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (1554)..(2726)
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223 <223> OTHER INFORMATION: Description of Artificial Sequence: Phaseolin promoter- pre-
pro-
224      chymosin-phaseolin terminator
226 <400> SEQUENCE: 3
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229 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
231 ttacttggtta ctttaatttc tcataatctt tgggtgaaat tatcacgctt ccgcacacga 180
233 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
235 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
237 agcggttggt gaaagcataa agattttatt ttattcttct tcatataaat gtttaatat 360
239 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
241 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
243 aatttaactc cataattttt ttattcgact gatcttaaag caacaccagc tgacacaact 540
245 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tataacaatga 600
247 aaatttcacc aaacaatcat ttgtgggtatt tctgaagcaa gtcattgtat gcaaaattct 660
249 ataattccca tttagacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
251 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaataactca 780
253 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
255 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
257 agtttaagat aaatataagt aatgtagtag agtgtagtag tgttacccta aaccataaac 960
259 tataacattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
261 atgtaagtcc gtaactagaa ttacagtggg ttgccatggc actctgtggg cttttgggtc 1080
263 atgcatgggt cttgcgcaag aaaaagacaa agaacaaaga aaaaagacaa aacagagaga 1140
265 caaaacgcaa tcacacaacc aactcaaatt agtcactggc tgatcaagat cgccgcgtcc 1200
267 atgtatgtct aaatgccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
269 ccatctcaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320
271 atatattcat tctcttcgcg cacctcaatt tcttcacttc aacacacgtc aacctgcata 1380
273 tgcggtgcat cccatgccca aatctccatg catgttccaa ccacctctc tcttatataa 1440
275 tacctataaa tacctcta atcactcact tctttcatca tccatccatc cagagtacta 1500
277 ctactctact actataatac cccaacccaa ctcatattca atactactct act atg 1556
278
279
281 aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa 1604
282 Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
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286 Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu
287      20      25      30
289 tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta 1700
290 Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu
291      35      40      45
293 gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc 1748
294 Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser
295 50      55      60      65
297 ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt 1796
298 Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser
299      70      75      80
301 caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc 1844
302 Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr
303      85      90      95
305 gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac 1892
306 Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr
307      100      105      110
309 tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag 1940
310 Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys
311      115      120      125
313 tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt 1988
314 Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly
315 130      135      140      145
317 aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc 2036
318 Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser
319      150      155      160
321 aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca 2084
322 Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro
323      165      170      175
325 ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca 2132
326 Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala
327      180      185      190
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330 Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met
331      195      200      205
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338 Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser
339      230      235      240
341 tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac 2324
342 Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr
343      245      250      255
345 tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt gca 2372
346 Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala
347      260      265      270
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VERIFICATION SUMMARY

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